

O-64 - BLOOD-BASED GENE EXPRESSION PROFILES FOR CLASSIFICATION OF SUBSYNDROMAL SYMPTOMATIC DEPRESSION AND MAJOR DEPRESSIVE DISORDER

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Objective: The present study compared the expression profile and made the classification with the leukocytes by using whole-genome cRNA microarrays among patients with SSD, major depressive disorder (MDD) and healthy controls.

Methods: Gene expression profiling was conducted in peripheral blood leucocytes from drug-free first-episode subjects with SSD, MDD, and matched controls (8 subjects in each group) using global mRNA expression arrays. Support vector machines (SVMs) were utilized for training and testing on candidate signature expression profiles from signature selection step.

Results: We identified SSD and MDD gene signatures from blood-based gene expression profile and build a SSD- MDD disorder model with higher predictive power. Firstly, we identified 63 differentially expressed SSD signatures in contrast to control ($P < = 5.0E-4$) and 30 differentially expressed MDD signatures in contrast to control, respectively. Then, 123 gene signatures were identified with significantly differential expression level between SSD and MDD. Secondly, in order to conduct priority selection for biomarkers for SSD and MDD together, we selected top gene signatures from each group of pair-wise comparison results, and merged the signatures together to generate better profiles used for clearly classify SSD and MDD sets in the same time. In details, we tried different combination of signatures from the three pair-wise compartmental results and finally determined 48 gene expression signatures with 100% accuracy.

Conclusion: Blood cell-derived RNA may have significant value for performing diagnostic functions and identifying disease biomarkers in SSD and MDD. These 48 gene model could classify SSD, MDD, and healthy controls.